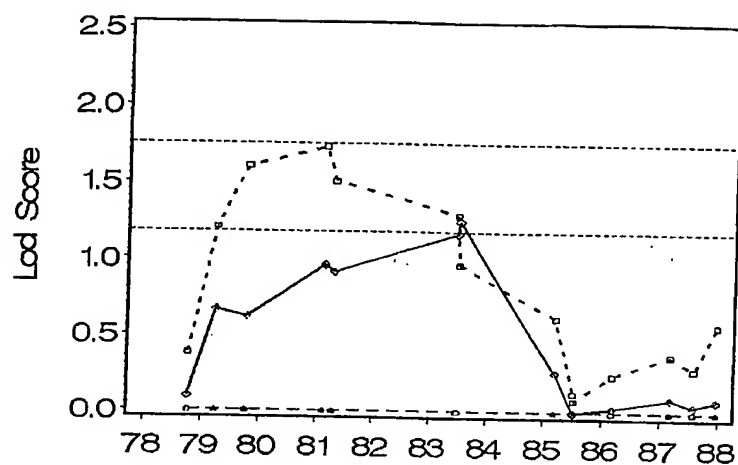


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A



B

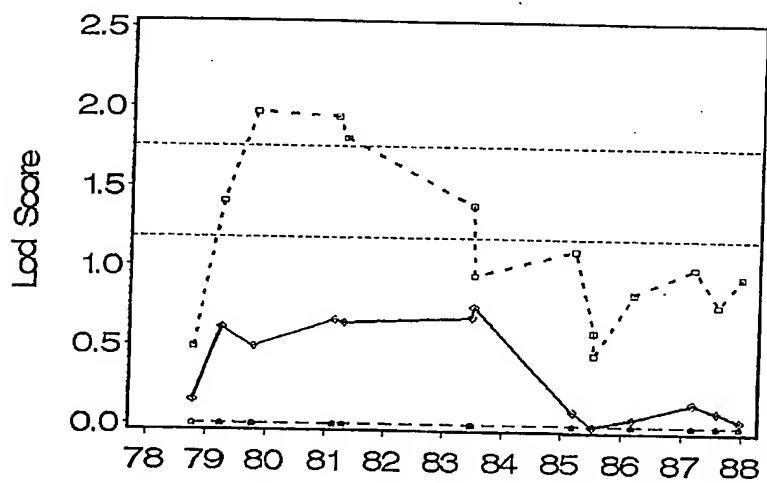


Fig. 1

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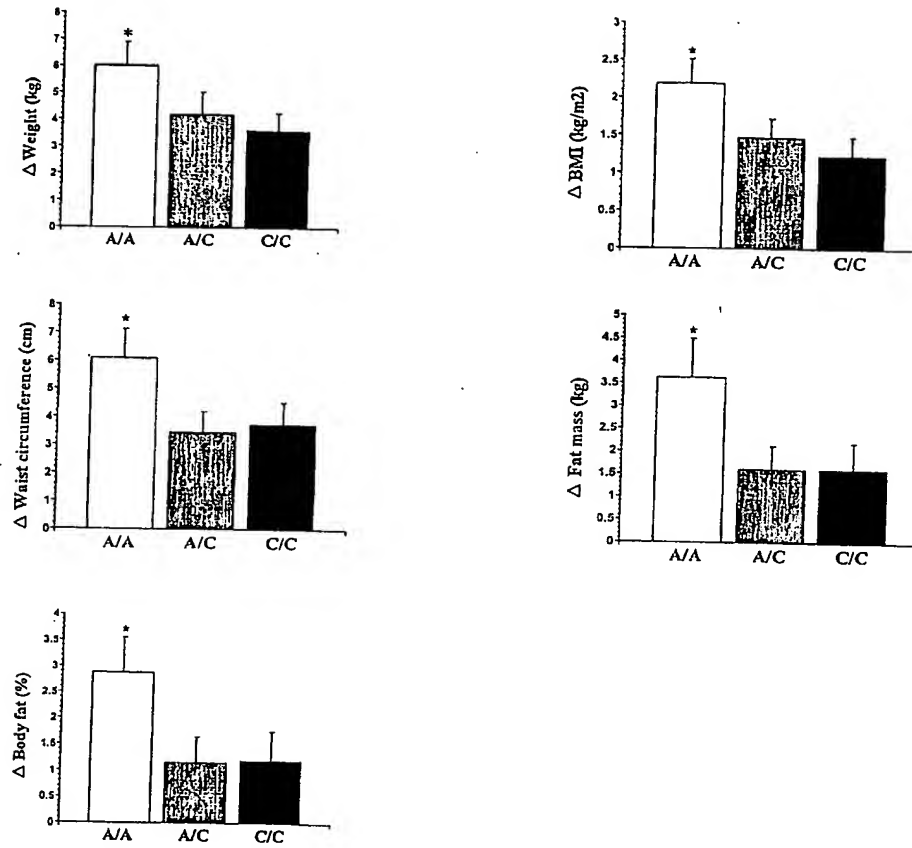


Fig. 2

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Homo sapiens

MARRAGGARMFGSLLL~~F~~ALLAAGVAPLSWDLPEPRSRASKIRVHSRGNLWATGHFMGKKS 60

Mus musculus

MTRQAGSSWLLRGLLL~~F~~ALFASGVAPFNWDLPEPRSRASKIRVHPRGNLWATGHFMGKKS 60

Homo sapiens

LEPSSPSPLGTAPH~~T~~SLRDQRLQLSHDLLGILLKKALGVSLSRPAPQIQYRLLVQILQK 121

Mus musculus

LEPPSLSLVGTAPPNTPRDQRLQLSHDLLRILLRKKALGMNFSGPAPPIQYRRLLEPLLQK 121

Fig. 3

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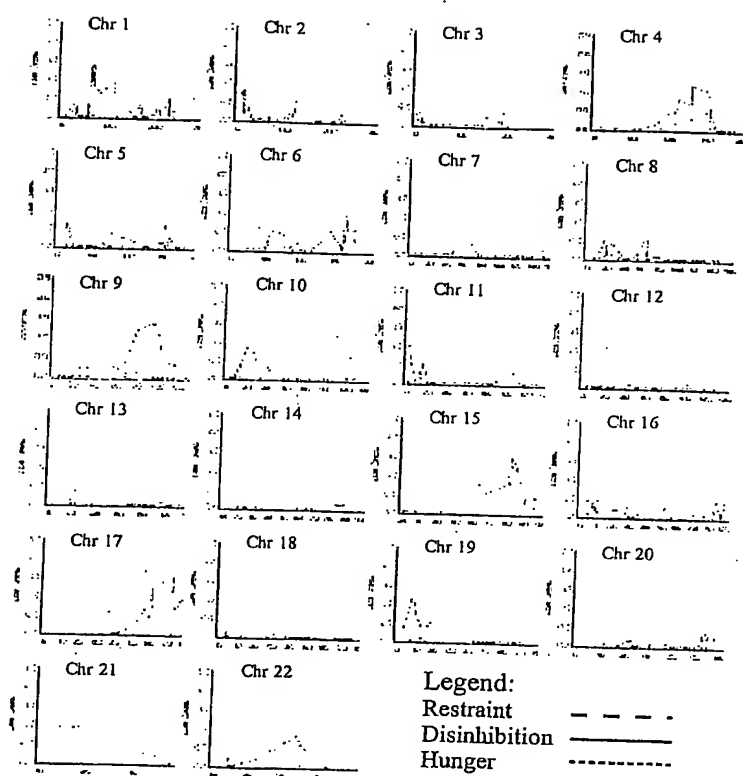


Fig. 4

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NMB_REF
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NMB_MUT
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NMB_REF
GGCTGAAGTGCCTATTGCGCCGAAAGCCGTGGCAGAGTGGCAAGGCAGGGCCAGGGGAAG 120
NMB_MUT
GGCTGAAGTGCCTATTGCGCCGAAAGCCGTGGCAGAGTGGCAAGGCAGGGCCAGGGGAAG

NMB_REF
CGGCTCCGCCCGCGGGGCGGGCCCTGTTTGGCCGGTGCCCGGTCCTTAGCCTGAAGGT 180
NMB_MUT
CGGCTCCGCCCGCGGGGCGGGCCCTGTTTGGCCGGTGCCCGGTCCTTAGCCTGAAGGT

NMB_REF
GGCGGGCTTCCGCCAGAAGCCCCTGGCGGAAGCGGTGCCCGGTGCGGGCCAGAGTGTGG 240
NMB_MUT
GGCGGGCTTCCGCCAGAAGCCCCTGGCGGAAGCGGTGCCCGGTGCGGGCCAGAGTGTGG

NMB_REF
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NMB_MUT
GTGTGCAGGTCTCTGGGCGGCCCAAAGGGGGTGCCCTGCCTGGTAACCTAGCGGGAGGG

NMB_REF
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NMB_MUT
TGGGGACGGCGGGGAGGGCGGCGGGCGGGGCACGGCTCCGCTGCTCAGGGCAGGCTCC

NMB_REF
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NMB_MUT
GCCCCAGGGGCGCGGATTTAAAAGGATCGAAGGCAGCCCCGAGCCCAGCGGCCGGGAA

NMB_REF
GCGCGCCCGAACGAAGCCGCGGCCCGGGCACAGCCATGGCCCGGCGGGCGGGGGGCGCTC 480
NMB_MUT
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NMB_REF
GGATGTTCCGGCAGCCTCCTGCTCTTCGCCCTGCTCGCTGCCGGCGTCGCCCCGCTCAGCT 540
NMB_MUT
GGATGTTCCGGCAGCCTCCTGCTCTTCGCCCTGCTCGCTGCCGGCGTCGCCCCGCTCAGCT

Fig. 5

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NMB_REF
GGGATCTCCCGAGCCCCGAGCCGAGCCAGCAAGATCCGAGTGCACTCGCGAGGCAACC 600
NMB_MUT
GGGATCTCCCGAGCCCCGAGCCGAGCCAGCAAGATCCGAGTGCACTCGCGAGGCAACC

NMB_REF
TCTGGGCCACCGGTAAGTCTTTGGGGACGGAGCAAGCAAGCGCCCCTCATCCAGTTCAGA 660
NMB_MUT
TCTGGGCCACCGGTAAGTCTTTGGGGACGGAGCAAGCAAGCGCCCCTCATCCAGTTCAGA

NMB_REF
CCCCATTTCTTCTCAACCCCTCTGGCCGCTCCTCAGCCACGGACACTAGTGTCGGAGCAG 720
NMB_MUT
CCCCATTTCTTCTCAACCCCTCTGGCCGCTCCTCAGCCACGGACACTAGTGTCGGAGCAG

NMB_REF
GTGGAAAACCCCTGGGGCTCATCTAATTTAATAGATATGTACTTGAGACCCGGACAGGTCA 780
NMB_MUT
GTGGAAAACCCCTGGGGCTCATCTAATTTAATAGATATGTACTTGAGACCCGGACAGGTCA

NMB_REF
GTGACTTGGCTAAGGTCGCGCAGCCAGTTTAAGACAGGGCTGGGCTAGATCCTAAATCCC 840
NMB_MUT
GTGACTTGGCTAAGGTCGCGCAGCCAGTTTAAGACAGGGCTGGGCTAGATCCTAAATCCC

NMB_REF
ACTGCCAGCCGGTGCCCCCTTACCTTAGGCGAGACTTAACCGAATCTTCTAACCGCTGGTG 900
NMB_MUT
ACTGCCAGCCGGTGCCCCCTTACCTTAGGCGAGACTTAACCGAATCTTCTAACCGCTGGTG

NMB_REF
TGTTTTTGCTGCACCTCCACTTTCCAGGCGCCTCTTCACTCTCCACTTCCTACCCTGCCC 960
NMB_MUT
TGTTTTTGCTGCACCTCCACTTTCCAGGCGCCTCTTCACTCTCCACTTCCTACCCTGCCC

NMB_REF
TTTTTCGTCCCTTGTCCTAAGCAGCCACACAAGTAGCAGAGTTTCTCCCTGGCCCTGGAC 1020
NMB_MUT
TTTTTCGTCCCTTGTCCTAAGCAGCCACACAAGTAGCAGAGTTTCTCCCTGGCCCTGGAC

NMB_REF
CATCCACCTTCTGCCAGCTGTGCCATCCTCTCTACCTGTTTCAGGAAAAGCTGAGGGAG 1080
NMB_MUT
CATCCACCTTCTGCCAGCTGTGCCATCCTCTCTACCTGTTTCAGGAAAAGCTGAGGGAG

Fig. 5 (cont')

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NMB_REF
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NMB_MUT
CAGGATTTGCCACCACCCAGACACCTTTGTGGCTCCTTGGTGAGGTGGAAGCACCAAGAG

NMB_REF
GAGGAAGGTTAAGTGTCTTCCCGCTACAAGAACGGAAACGTGGGAGAGATGAGGAACTTT 1200
NMB_MUT
GAGGAAGGTTAAGTGTCTTCCCGCTACAAGAACGGAAACGTGGGAGAGATGAGGAACTTT

NMB_REF
TCCTCTGAGGTAGGATCCTGGCTGCTTGACTTCCTTGTGCCTGGACACCTCCTTTCCAGG 1260
NMB_MUT
TCCTCTGAGGTAGGATCCTGGCTGCTTGACTTCCTTGTGCCTGGACACCTCCTTTCCAGG

NMB_REF
TCACTTCATGGGCAAGAAGAGTCTGGAGCCTTCCAGCCCATCCCCATTGGGGACAGCTCC 1320
NMB_MUT
TCACTTCATGGGCAAGAAGAGTCTGGAGCCTTCCAGCCCATCCCCATTGGGGACAGCTAC

NMB_REF
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NMB_MUT
CCAACCTCCCTGAGGGACCAGCGACTGCAGCTGAGTCATGATCTGCTCGGAATCCTCCT

NMB_REF
GCTAAAGAAGGCTCTGGGCGTGAGCCTCAGCCGCCCGCACCCCAAATCCAGGTGAGCCG 1440
NMB_MUT
GCTAAAGAAGGCTCTGGGCGTGAGCCTCAGCCGCCCGCACCCCAAATCCAGGTGAGCCG

NMB_REF
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NMB_MUT
GGCCCCTGCTCCAATGTCAGGAGGGCCAGCTGGGGCCATCCCCGGATCCTGCATGGAAG

NMB_REF
GAATTACCACCCAGTACTGTATTAGGGTGTGACTGTCTGACTAGGACATTATGGGTGTGG 1560
NMB_MUT
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NMB_REF
ACCCAGAAAAGCCAGGTTTCCAGGCTTTCCCTCTTGAGGCAGAGCTCAAAGGAGGAACA 1620
NMB_MUT
ACCCAGAAAAGCCAGGTTTCCAGGCTTTCCCTCTTGAGGCAGAGCTCAAAGGAGGAACA

Fig. 5 (cont')

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NMB_REF
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NMB_MUT
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NMB_REF
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NMB_MUT
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NMB_REF
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NMB_MUT
CAGGACCTTTCTCCCCAGTCTACACAGTCTTGTCCCACCCATGCTGTTCCCTGCTGCAT

NMB_REF
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NMB_MUT
TAGTCAAGTCCACCTTTGCTGTGCTCCTGTGTATGCTTGTGGCCGGAATGGGACCCTGAGG

NMB_REF
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NMB_MUT
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NMB_REF
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NMB_MUT
TGGAGCTCTTCCCATTTCTCTCATCTGCCTCAGTATCCAGTGGTAGGGTTTAGCAACTTCA

NMB_REF
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NMB_MUT
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NMB_REF
GGATGTTTGGCAGCATCCCTGGTCTCTACATACTAGATGCCAGTAGCATCTTTCCCCCCC 2100
NMB_MUT
GGATGTTTGGCAGCATCCCTGGTCTCTACATACTAGATGCCAGTAGCATCTTTCCCCCCC

NMB_REF
ATCAAGTTGTGACAACTGAAAAGACCTCCAGACATCACCAGATGTCTGCTGGGGGAGAGG 2160
NMB_MUT
ATCAAGTTGTGACAACTGAAAAGACCTCCAGACATCACCAGATGTCTGCTGGGGGAGAGG

Fig. 5 (cont')

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NMB_MUT
GCCCAAATCATTATTGGTTGTCAGTCACTGATCTATGGGATTCAAGACTCCAAAGCTGG

NMB_REF
AGCCAAGCTAGCCTCAAGGTATAGCCCCGCTGAGTGGCAACTCCTTCATTCCCTGCTCCT 2280
NMB_MUT
AGCCAAGCTAGCCTCAAGGTATAGCCCCGCTGAGTGGCAACTCCTTCATTCCCTGCTCCT

NMB_REF
GGTGCTGTCCTTACTGCACACCACCCTCCCTGGTCCTGCTGCTGTGTGCAGAAGGCAGTG 2340
NMB_MUT
GGTGCTGTCCTTACTGCACACCACCCTCCCTGGTCCTGCTGCTGTGTGCAGAAGGCAGTG

NMB_REF
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NMB_MUT
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NMB_REF
TAGCTGTATGACCTTAGAAATGTCCCTTAACCTCTCTAAAGCCTCAATATTCTTCACCCA 2460
NMB_MUT
TAGCTGTATGACCTTAGAAATGTCCCTTAACCTCTCTAAAGCCTCAATATTCTTCACCCA

NMB_REF
TAAAATGAAGATAATAAGGCCCATCTCCATTAAATGAGACCATTTATGTCAAATGCTCA 2520
NMB_MUT
TAAAATGAAGATAATAAGGCCCATCTCCATTAAATGAGACCATTTATGTCAAATGCTCA

NMB_REF
GCATGGTGCCTGGCTCATAGACAGCCCTTAGTAGATGCGAGCTCTTATCAGTCTGTGAGC 2580
NMB_MUT
GCATGGTGCCTGGCTCATAGACAGCCCTTAGTAGATGCGAGCTCTTATCAGTCTGTGAGC

NMB_REF
TCCCTGGCGGCACCTGTTGTAGACTCGCCTTCATATCCCCCAGTGTGCCTAGCATATAGT 2640
NMB_MUT
TCCCTGGCGGCACCTGTTGTAGACTCGCCTTCATATCCCCCAGTGTGCCTAGCATATAGT

NMB_REF
GTGTGCATTTTGAAGGGAGAGGCATTCCCTAGAAAAGGTCCAACCCAGCCTCAACCAACA 2700
NMB_MUT
GTGTGCATTTTGAAGGGAGAGGCATTCCCTAGAAAAGGTCCAACCCAGCCTCAACCAACA

Fig. 5 (cont')

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NMB_REF
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NMB_MUT
TCCCTGACTTCCTGAGGCACAGAACCAGCAGCCCCTGAGGACCTCAGATGTAAGGCCTAG

NMB_REF
GAGCTTGGGCTGGCTGAGTCTGAAGGGAAACAATGTCACCTCTAATGCCCTTGTTTTGA 2820
NMB_MUT
GAGCTTGGGCTGGCTGAGTCTGAAGGGAAACAATGTCACCTCTAATGCCCTTGTTTTGA

NMB_REF
AGCTCTGACACATGCAGACCAACTAGAGAATCTCAGAAGCAGCAGTGCCTACGTCTGGGG 2880
NMB_MUT
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NMB_REF
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NMB_MUT
CTTCAGAGTGAGGTCTGGGGCAGAGCTGGGGTGGGGGAGTGAGGACGCTGACACTAGCCC

NMB_REF
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NMB_MUT
AGCACCAGCACTGTATTTGGATTTTCTTCCACGATCTTCTTTGACTGTCATGACCACCC

NMB_REF
TGGGTGGTTGGGGCTGTGTTCTGAGAAAACTACTGCCCCGACCCCTCCAAGGCAATTCAG 3060
NMB_MUT
TGGGTGGTTGGGGCTGTGTTCTGAGAAAACTACTGCCCCGACCCCTCCAAGGCAATTCAG

NMB_REF
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NMB_MUT
GGTGCTCTGGGGCCTGCCTCAGCTGACAGCCTGCTGGTGCCACCTCTGCAGACATCTGG

NMB_REF
CACTTAGGAATGGCAGGATGCCCCATCTTTATCAGGAGCCCCTCCCTGGCTCAATTCTT 3180
NMB_MUT
CACTTAGGAATGGCAGGATGCCCCATCTTTATCAGGAGCCCCTCCCTGGCTCAATTCTT

NMB_REF
CTGTATGTTTCTCTTCAGTACAGGAGGCTGCTGGTACAAATACTGCAGAAATGACACCAA 3240
NMB_MUT
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Fig. 5 (cont')

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NMB_MUT
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NMB_REF
GGACCCTGTTGATGGCCCCATCTGGATGTAAATCCTGAGCTCAAATCTCTGTTACTCCAT 3360
NMB_MUT
GGACCCTGTTGATGGCCGCATCTGGATGTAAATCCTGAGCTCAAATCTCTGTTACTCCAT

NMB_REF
TACTGTGATTTCTGGCTGGGTCAACCAGAAATATCGCTGATGCAGACACAGATTATGTTCC 3420
NMB_MUT
TACTGTGATTTCTGGCTGGGTCAACCAGAAATATCGCTGATGCAGACACAGATTATGTTCC

NMB_REF
TGCTGTATTTCTGCTTCCCTGTTGAATTGGTGAATAAAACCTTGCTCTTTACATACAAT 3480
NMB_MUT
TGCTGTATTTCTGCTTCCCTGTTGAATTGGTGAATAAAACCTTGCTCTTTACATAAAAT

NMB_REF
GCCTGGTCCTCTCCTTTCACCCGTCCTTTAGGGGATGGGAGGAAAAGGGGGCTGGAGGGC 3540
NMB_MUT
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NMB_REF
AGAGTGTTCAGTGAGATGGGGCTGGCTCAAAAAGTCCAGAATACCCCATGCCATGGCACC 3600
NMB_MUT
AGAGTGTTCAGTGAGATGGGGCTGGCTCAAAAAGTCCAGAATACCCCATGCCATGGCACC

NMB_REF
AGCCTGGCACTGACTCTGGCCTCCTACCCATTCAATTCAGCAAGCAAATAACGCCTGTTGC 3660
NMB_MUT
AGCCTGGCACTGACTCTGGCCTCCTACCCATTCAATTCAGCAAGCAAATAACGCCTGTTGC

NMB_REF ATGCCAGGCTTCGTGCC 3677
NMB_MUT ATGCCAGGCTTCGTGCC

Fig. 5 (cont:')

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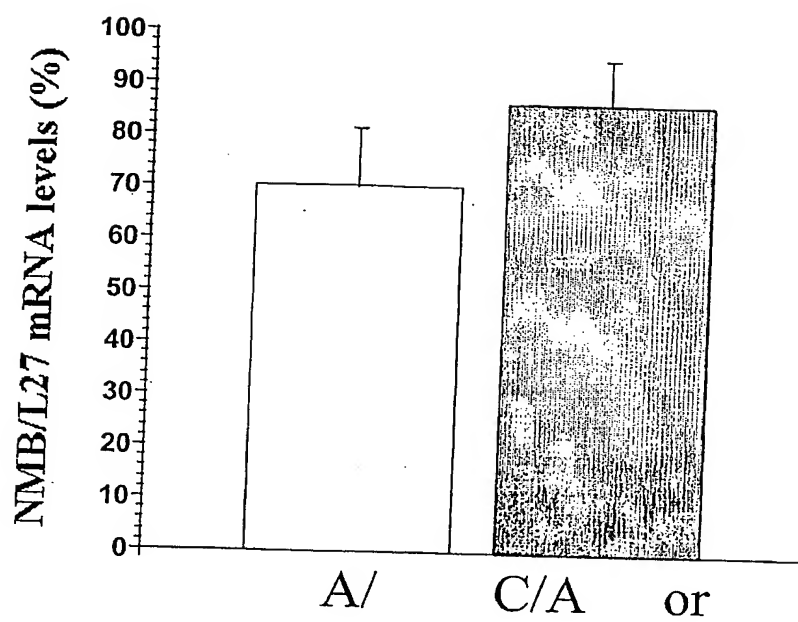


Fig. 6

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g.433 C>T or rs1849288 (within NMB promoter)

NMB_REF

CTGTTACCCGGGAGGAGAGCTCCTCGCCCGACCTCTACCCTCATGAAGAGAGGCTCAGAG

NMB_MUT

CTGTTACCCGGGAGGAGAGCTCTTCGCCCGACCTCTACCCTCATGAAGAGAGGCTCAGAG

g.438 C>G or IVS1+281 C>G or rs2175567 (within NMB intron 1)

NMB_REF

TTACCTTAGGCGAGACTTAACCGAATCTTCTAACCGCTGGTGTGTTTTTGCTGCACCTCC

NMB_MUT

TTACCTTAGGCGAGACTTAACCGAATCTTCTAACGGCTGGTGTGTTTTTGCTGCACCTCC

g.630 C>A or IVS1+473 C>A or rs2292462 (within NMB intron 1)

NMB_REF

GGAAAAGCTGAGGGAGCAGGCTTGGCCACCACCCAGACACCTTTGTGGCTCCTTGGTGAG

NMB_MUT

GGAAAAGCTGAGGGAGCAGGATTTGCCACCACCCAGACACCTTTGTGGCTCCTTGGTGAG

g.864 C>A or c.217 C>A (position on the coding sequence (cDNA) from the NMB first codon) or p.P73T (within NMB exon 2) or rs1051168

NMB_REF

CCAGCCCATTCCCCATTGGGGACAGCTCCCCACACCTCCCTGAGGGACCAGCGACTGCAGC

NMB_MUT

CCAGCCCATTCCCCATTGGGGACAGCTACCCACACCTCCCTGAGGGACCAGCGACTGCAGC

g.1043 G>A or IVS2+66 G>A (unknown in databases) (within NMB intron 2)

NMB_REF

GGCCATCCCCGGATCCTGCATGGGAGGAATTACCACCCAGTACTGTATTAGGGTGTGACT

NMB_MUT

GGCCATCCCCGGATCCTGCATGGAAGGAATTACCACCCAGTACTGTATTAGGGTGTGACT

g.1173 G>C or IVS2+196 G>C(unknown in databases) (within NMB intron 2)

NMB_REF

GCAGAGCTCAAAGGAGGAACAGTCCAAAGAAAGGAAGCTGACCTTCCCAGTAGACCCCAT

NMB_MUT

GCAGAGCTCAAAGGAGGAACAGTCCAAACAAAGGAAGCTGACCTTCCCAGTAGACCCCAT

g.2493 A>G or IVS2-251 A>G or rs3809508 (within NMB intron 2)

NMB_REF

GTGAGGACGCTGACACTAGCCCAGCACCAAGCACTGTATTGGATTTTCTTCCACGATCT

NMB_MUT

GTGAGGACGCTGACACTAGCCCAGCACCAAGCACTGTATTGGATTTTCTTCCACGATCT

Fig. 7

7/7

g.2708 C>T or IVS2-36 C>T (unknown in databases) (within NMB intron 2)

NMB_REF

AATGGCAGGATGCCCCTATCTTTATCAGGAGCCCCTCCCTGGCTCAATTCTTCTGTATGT

NMB_MUT

AATGGCAGGATGCCCCTATCTTTATCAGGAGCCCCTCCCTGGCTCAATTCTTCTGTATGT

g.2817 T>C or g.*38 T>C or rs3748371 (within NMB 3' untranslated region)

NMB_REF

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NMB_MUT

TAATGGGGCAGACACAACAGCGTGGCTTAGACTGTGCCACCCAGGGAAGGTGCTGAATG

g.2863 C>G or g.*84 C>G or rs1804012 (within NMB 3' untranslated region)

NMB_REF

GTGCTGAATGGGACCCTGTTGATGGCCCCATCTGGATGTAAATCCTGAGCTCAAATCTCT

NMB_MUT

GTGCTGAATGGGACCCTGTTGATGGCCGCATCTGGATGTAAATCCTGAGCTCAAATCTCT

g.3022 C>A or g.*243 C>A or rs3748372 (within NMB 3' untranslated region)

NMB_REF

ATAAAACCTTGCTCTTTACATACAATGCCTGGTCCTCTCCTTTACCCGTCTTTAGGGG

NMB_MUT

ATAAAACCTTGCTCTTTACATAAAATGCCTGGTCCTCTCCTTTACCCGTCTTTAGGGG

Fig. 7 (cont')